

SEQUENCE LISTING

<110> CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE, INC.

<120> Novel G protein-coupled receptors

<130> C2-012DP1PCT

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<150> JP 1998-288565

<151> 1998-10-09

<150> JP 1998-347546

<151> 1998-12-07

<150> JP 1998-363537

<151> 1998-12-21

<160> 53

<170> PatentIn version 2.0

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (9)..(947)

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ttg gga ctc act gat aac cgg gtg ctg gaa atg ctg ttt ttc atg gca 98

Leu Gly Leu Thr Asp Asn Arg Val Leu Glu Met Leu Phe Phe Met Ala

15 20 25 30

ttc tca gcc att tat atg cta acg ctt tca ggg aac att ctc atc atc 146

Phe Ser Ala Ile Tyr Met Leu Thr Leu Ser Gly Asn Ile Leu Ile Ile

35 40 45

att gcc aca gtc ttt act cca agt ctc cat acc ccc atg tat ttc ttc 194

Ile Ala Thr Val Phe Thr Pro Ser Leu His Thr Pro Met Tyr Phe Phe

50 55 60

ctg agc aat ctg tcc ttt att gac atc tgc cac tca tct gtc act gtg 242

Leu Ser Asn Leu Ser Phe Ile Asp Ile Cys His Ser Ser Val Thr Val

65 70 75

cct aag atg ttg gag ggt ttg ctt tta gaa aga aag acc att tcc ttt 290

Pro Lys Met Leu Glu Gly Leu Leu Leu Glu Arg Lys Thr Ile Ser Phe

80 85 90

gac aac tgc atc aca cag ctc ttc ttc cta cat ctc ttt gcc tgt gcc 338

Asp Asn Cys Ile Thr Gln Leu Phe Phe Leu His Leu Phe Ala Cys Ala

95 100 105 110

gag atc ttt ctg ctg atc att gtg gcg tat gat cgt tac gtg gct atc 386

Glu Ile Phe Leu Leu Ile Ile Val Ala Tyr Asp Arg Tyr Val Ala Ile

115 120 125

tgc act cca ctc cac tac ccc aat gtg atg aac atg aga gtc tgt ata 434

Cys Thr Pro Leu His Tyr Pro Asn Val Met Asn Met Arg Val Cys Ile

130 135 140

cag ctt gtc ttt gct ctc tgg ttg ggg ggt act gtt cac tca cta ggg 482

Gln Leu Val Phe Ala Leu Trp Leu Gly Gly Thr Val His Ser Leu Gly

145 150 155

cag acc ttc ttg act att cgt cta cct tac tgt ggc ccc aac att att 530

Gln Thr Phe Leu Thr Ile Arg Leu Pro Tyr Cys Gly Pro Asn Ile Ile

160 165 170

gac agc tac ttc tgt gat gtg cct ctt gtt atc aag ctg gcc tgc aca 578

Asp Ser Tyr Phe Cys Asp Val Pro Leu Val Ile Lys Leu Ala Cys Thr

175 180 185 190

gat aca tac ctc aca gga ata ctg att gtg acc aat agt gga acc atc 626

Asp Thr Tyr Leu Thr Gly Ile Leu Ile Val Thr Asn Ser Gly Thr Ile

195 200 205

tcc ctc tcc tgt ttc ttg gcc gtg gtc acc tcc tat atg gtc atc ctg 674

Ser Leu Ser Cys Phe Leu Ala Val Val Thr Ser Tyr Met Val Ile Leu

210 215 220

gtt tct ctt cga aaa cac tca gct gaa ggg cgc cag aaa gcc ctg tct 722

Val Ser Leu Arg Lys His Ser Ala Glu Gly Arg Gln Lys Ala Leu Ser

225 230 235
 acc tgc tgc gcc cac ttc atg gtg gtt gcc ctc ttc ttt ggg cca tgt 770
 Thr Cys Ser Ala His Phe Met Val Val Ala Leu Phe Phe Gly Pro Cys
 240 245 250
 atc ttc atc tat act cgg cca gac acc agc ttc tcc att gac aag gtg 818
 Ile Phe Ile Tyr Thr Arg Pro Asp Thr Ser Phe Ser Ile Asp Lys Val
 255 260 265 270
 gtg tct gtc ttc tac aca gtg gtc acc cct ttg ctg aat ccc ttc att 866
 Val Ser Val Phe Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Phe Ile
 275 280 285
 tac acc ttg agg aat gag gag gta aaa agt gcc atg aag cag ctc agg 914
 Tyr Thr Leu Arg Asn Glu Glu Val Lys Ser Ala Met Lys Gln Leu Arg
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 cag aga caa gtt ttt ttc acg aaa tca tat aca taatgggcat tgggattgca 967
 Gln Arg Gln Val Phe Phe Thr Lys Ser Tyr Thr
 305 310
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 tataacttgg taaattaggt aaaatggcat agagcaggtc agatttctgc tcattaaaga 1087
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<222> (13).. (951)

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Leu Thr Gly Ile Pro Tyr Pro Leu Arg Leu Arg Thr Leu Phe Phe Val

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25

ttc ttt ttt cta atc tac atc ctg act cag ctg gga aac ctg ctt att 147

Phe Phe Phe Leu Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile

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35

40

45

tta atc act gtc tgg gca gac cca agg ctc cat gcc cgc ccc atg tac 195

Leu Ile Thr Val Trp Ala Asp Pro Arg Leu His Ala Arg Pro Met Tyr

50

55

60

atc ttt ctt ggt gtt ctc tca gtc att gat atg agc atc tcc tcc atc 243

Ile Phe Leu Gly Val Leu Ser Val Ile Asp Met Ser Ile Ser Ser Ile

65

70

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att gtc cct cgc ctc atg atg aac ttc act tta ggt gtc aaa ccc atc 291

Ile Val Pro Arg Leu Met Met Asn Phe Thr Leu Gly Val Lys Pro Ile

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cca ttt ggt ggc tgt gtt gct caa ctc tat ttc tat cac ttc ctg ggc 339

Pro Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Tyr His Phe Leu Gly

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Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu

110 115 120 125
gca ata tgt cag ccc ctg cgc tac cct gtg ctc atg act gct aag ctg 435
Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Thr Ala Lys Leu
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agc gcc ttg ctt gtg gct gga gcc tgg atg gca gga tcc atc cat ggg 483
Ser Ala Leu Leu Val Ala Gly Ala Trp Met Ala Gly Ser Ile His Gly
145 150 155
gct ctc cag gcc atc cta acc ttc cgc ctg ccc tac tgt ggg ccc aat 531
Ala Leu Gln Ala Ile Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro Asn
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cag gtg gat tac ttc ttc tgt gac atc cct gca gtg ttg aga ctg gcc 579
Gln Val Asp Tyr Phe Phe Cys Asp Ile Pro Ala Val Leu Arg Leu Ala
175 180 185
tgt gct gac aca aca gtc aac gag ctg gtg acg ttt gta gac att ggg 627
Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile Gly
190 195 200 205
gtg gtg gtt gcc agt tgc ttc tcc ctg atc ctc ctc tcc tac ata cag 675
Val Val Val Ala Ser Cys Phe Ser Leu Ile Leu Leu Ser Tyr Ile Gln
210 215 220
atc att cag gcc atc ctg aga atc cac aca gct gat ggg cgg cgc cgg 723
Ile Ile Gln Ala Ile Leu Arg Ile His Thr Ala Asp Gly Arg Arg Arg
225 230 235
gct ttt tca act tgt gga gcc cat gta acc gtg gtc acc gtg tac tat 771
Ala Phe Ser Thr Cys Gly Ala His Val Thr Val Val Thr Val Tyr Tyr
240 245 250
gtg ccc tgt gcc ttc atc tac ctg agg cct gaa acc aac agc ccc ctg 819

Val Pro Cys Ala Phe Ile Tyr Leu Arg Pro Glu Thr Asn Ser Pro Leu

255

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Asp Gly Ala Ala Ala Leu Val Pro Thr Ala Ile Thr Pro Phe Leu Asn

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ccc ctt atc tac act ctg cgg aac caa gag gtg aag ctg gcc ctg aaa 915

Pro Leu Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Leu Ala Leu Lys

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aga atg ctc aga agc cca aga act ccg agt gag gtt tgaaagtgtc 961

Arg Met Leu Arg Ser Pro Arg Thr Pro Ser Glu Val

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gtttaaggta aaataactaac ttcttaacag ttccttagta tcctctcaag ataactctca 1141

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 gaactaaagc gaggttaatt tccacagtga gaacatgctc cagacatccg agcaccagtg 240
 tggtcttgga aactccacag ataccacagg actagaaaat aactggacaa tgggatgttc 300
 tatcttggcc gaactgaggg atataaaaag ctccaaagac aaagaaagta ccatccaccc 360
 atcccaaaag aaattatcct tccttctgaa aataagactg caaaaagac atg gga aag 418

Met Gly Lys

1

acc aaa aac aca tcg ctg gat gcc gtg gtg aca gat ttc att ctt ctg 466

Thr Lys Asn Thr Ser Leu Asp Ala Val Val Thr Asp Phe Ile Leu Leu

5

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ggg ttg tct cac ccc cca aat cta aga agc ctc ctc ttc ctg gtc ttc 514

Gly Leu Ser His Pro Pro Asn Leu Arg Ser Leu Leu Phe Leu Val Phe

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35

ttc atc att tac atc ctc act cag ctg ggg aac ctg ctc att ctg ctc 562

Phe Ile Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile Leu Leu

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acc atg tgg gct gac ccg aag ctc tgt gct cgc ccc atg tac att ctt 610

Thr Met Trp Ala Asp Pro Lys Leu Cys Ala Arg Pro Met Tyr Ile Leu

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ctg gga gtg ctc tca ttc ctg gac atg tgg ctc tcc tca gtc acc gtt 658

Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser Val Thr Val

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cct cgg ctt att ttg gat ttt act cct tcc atc aag gct atc ccg ttt 706

Pro Arg Leu Ile Leu Asp Phe Thr Pro Ser Ile Lys Ala Ile Pro Phe

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90

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ggt ggc tgt gtg gct caa ctg tat ttc ttt cac ttc ctg ggc agc acc 754
 Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Ser Thr
 100 105 110 115
 cag tgc ttc ctc tac acc ttg atg gcc tat gac agg tac cta gca ata 802
 Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu Ala Ile
 120 125 130
 tgt cag ccc ctg cac tac cca gtg ctc atg aat ggg agg tta tgc aca 850
 Cys Gln Pro Leu His Tyr Pro Val Leu Met Asn Gly Arg Leu Cys Thr
 135 140 145
 gtc ctt gtg gct gga gct tgg gtc gcc ggc tcc atg cat ggg tct atc 898
 Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His Gly Ser Ile
 150 155 160
 cag gcc acc ttg acc ttc cgc ctg ccc tac tgt ggg ccc aat cag gtg 946
 Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro Asn Gln Val
 165 170 175
 gat tac ttt atc tgt gac atc cgc gca gta ttg aga ctg gcc tgt gct 994
 Asp Tyr Phe Ile Cys Asp Ile Arg Ala Val Leu Arg Leu Ala Cys Ala
 180 185 190 195
 gac aca act gtc aat gag ctt gtg acc ttt gtg gac gtc agg gta gtg 1042
 Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val Arg Val Val
 200 205 210
 gcc gcc agt tgc ttc atg tta att ctg ctc tcc tat gcc aac ata gtc 1090
 Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala Asn Ile Val
 215 220 225
 cat gcc atc ctg aag ata cgc acc gct gat ggg agg cgc cgg gcc ttc 1138
 His Ala Ile Leu Lys Ile Arg Thr Ala Asp Gly Arg Arg Arg Ala Phe

10/66

230 235 240
 tcc acc tgt ggc tcc cac cta atc gtg gtc aca gtc tac tat gtc ccc 1186
 Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr Tyr Val Pro
 245 250 255
 tgt att ttc atc tac ctt agg gct ggc tcc aaa gac ccc ctg gat ggg 1234
 Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Asp Pro Leu Asp Gly
 260 265 270 275
 gca gcg gct gtg ttt tac act gtt gtc act cca tta ctg aac ccc ctc 1282
 Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Leu
 280 285 290
 atc tat aca ctg agg aac cag gaa gtg aag tct gcc ctg aag agg ata 1330
 Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Ser Ala Leu Lys Arg Ile
 295 300 305
 aca gca ggt tgaaggactg aatgaaaata agtaactaca tctgcatcat 1379
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Leu Thr Asp Asn Arg Val Leu Glu Met Leu Phe Phe Met Ala Phe Ser

11/66

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Ala Ile Tyr Met Leu Thr Leu Ser Gly Asn Ile Leu Ile Ile Ala		
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Thr Val Phe Thr Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Ser		
50	55	60
Asn Leu Ser Phe Ile Asp Ile Cys His Ser Ser Val Thr Val Pro Lys		
65	70	75
Met Leu Glu Gly Leu Leu Leu Glu Arg Lys Thr Ile Ser Phe Asp Asn		
85	90	95
Cys Ile Thr Gln Leu Phe Phe Leu His Leu Phe Ala Cys Ala Glu Ile		
100	105	110
Phe Leu Leu Ile Ile Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys Thr		
115	120	125
Pro Leu His Tyr Pro Asn Val Met Asn Met Arg Val Cys Ile Gln Leu		
130	135	140
Val Phe Ala Leu Trp Leu Gly Gly Thr Val His Ser Leu Gly Gln Thr		
145	150	155
Phe Leu Thr Ile Arg Leu Pro Tyr Cys Gly Pro Asn Ile Ile Asp Ser		
165	170	175
Tyr Phe Cys Asp Val Pro Leu Val Ile Lys Leu Ala Cys Thr Asp Thr		
180	185	190
Tyr Leu Thr Gly Ile Leu Ile Val Thr Asn Ser Gly Thr Ile Ser Leu		
195	200	205
Ser Cys Phe Leu Ala Val Val Thr Ser Tyr Met Val Ile Leu Val Ser		
210	215	220
Leu Arg Lys His Ser Ala Glu Gly Arg Gln Lys Ala Leu Ser Thr Cys		

12/66

225 230 235 240
 Ser Ala His Phe Met Val Val Ala Leu Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Thr Arg Pro Asp Thr Ser Phe Ser Ile Asp Lys Val Val Ser
 260 265 270
 Val Phe Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Phe Ile Tyr Thr
 275 280 285
 Leu Arg Asn Glu Glu Val Lys Ser Ala Met Lys Gln Leu Arg Gln Arg
 290 295 300
 Gln Val Phe Phe Thr Lys Ser Tyr Thr
 305 310

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<212> PRT

<213> Homo sapiens

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 Leu Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile Leu Ile Thr
 35 40 45
 Val Trp Ala Asp Pro Arg Leu His Ala Arg Pro Met Tyr Ile Phe Leu
 50 55 60
 Gly Val Leu Ser Val Ile Asp Met Ser Ile Ser Ser Ile Ile Val Pro

65	70	75	80
Arg Leu Met Met Asn Phe Thr Leu Gly Val Lys Pro Ile Pro Phe Gly			
	85	90	95
Gly Cys Val Ala Gln Leu Tyr Phe Tyr His Phe Leu Gly Ser Thr Gln			
	100	105	110
Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys			
	115	120	125
Gln Pro Leu Arg Tyr Pro Val Leu Met Thr Ala Lys Leu Ser Ala Leu			
	130	135	140
Leu Val Ala Gly Ala Trp Met Ala Gly Ser Ile His Gly Ala Leu Gln			
	145	150	155
Ala Ile Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro Asn Gln Val Asp			
	165	170	175
Tyr Phe Phe Cys Asp Ile Pro Ala Val Leu Arg Leu Ala Cys Ala Asp			
	180	185	190
Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile Gly Val Val Val			
	195	200	205
Ala Ser Cys Phe Ser Leu Ile Leu Leu Ser Tyr Ile Gln Ile Ile Gln			
	210	215	220
Ala Ile Leu Arg Ile His Thr Ala Asp Gly Arg Arg Arg Ala Phe Ser			
	225	230	235
Thr Cys Gly Ala His Val Thr Val Val Thr Val Tyr Tyr Val Pro Cys			
	245	250	255
Ala Phe Ile Tyr Leu Arg Pro Glu Thr Asn Ser Pro Leu Asp Gly Ala			
	260	265	270
Ala Ala Leu Val Pro Thr Ala Ile Thr Pro Phe Leu Asn Pro Leu Ile			

275 280 285
 Tyr Thr Leu Arg Asn Gln Glu Val Lys Leu Ala Leu Lys Arg Met Leu
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 Arg Ser Pro Arg Thr Pro Ser Glu Val
 305 310

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<213> Homo sapiens

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 35 40 45
 Ile Leu Leu Thr Met Trp Ala Asp Pro Lys Leu Cys Ala Arg Pro Met
 50 55 60
 Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser
 65 70 75 80
 Val Thr Val Pro Arg Leu Ile Leu Asp Phe Thr Pro Ser Ile Lys Ala
 85 90 95
 Ile Pro Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu
 100 105 110
 Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr

15/66

115	120	125	
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130	135	140	
Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His			
145	150	155	160
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro			
165	170	175	
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Arg Ala Val Leu Arg Leu			
180	185	190	
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val			
195	200	205	
Arg Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala			
210	215	220	
Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Ala Asp Gly Arg Arg			
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Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr			
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Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Asp Pro			
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Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu			
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19/66

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AGCTTCACCT CTTGGTTCCG CAGAGTG 27

<210> 17

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 caactctatt tctatcactt cctgggcagc acccagtgt tctctacac cctaattggc 360
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 gacatccctg cagtgttgag actggcctgt gctgacacaa cagtcaacga gctggtgacg 600
 tttgtagaca ttgggggtgt ggttgccagt tgcttctccc tgatcctcct ctcctacata 660
 cagatcattc aggccatcct gagaatccac acagctgatg ggcggcgcgc ggctttttca 720
 acttgtggag cccatgtaac cgtggtcacc gtgtactatg tgccctgtgc cttcatctac 780
 ctgaggcctg aaaccaacag cccctggat ggggcagctg ccctagtccc cacggccatc 840
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 aaaagaatgc tcagaagccc aagaactccg agtgaggttt ga 942

<210> 23

<211> 933

<212> DNA

<213> Homo sapiens

<400> 23

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 ctactcagc tggggaacct gctcattctg ctcacatgt gggctgaccc gaagctctgt 180
 gctcgcccca tgtacattct tctgggagtg ctctcattcc tggacatgtg gctctcctca 240
 gtcaccgttc ctcggttat tttggatttt actccttcca tcaaggctat cccgttttgt 300

ggctgtgtgg ctcaactgta tttctttcac ttcctgggca gcacccagtg cttcctctac 360
 accttgatgg cctatgacag gtacctagca atatgtcagc ccctgcacta cccagtgtc 420
 atgaatggga gggttatgcac agtccttgtg gctggagctt gggtcgccgg ctccatgcat 480
 gggctctatcc aggccacctt gaccttcgc ctgccctact gtgggcccac tcaggtggat 540
 tactttatct gtgacatccg cgcagtattg agactggcct gtgctgacac aactgtcaat 600
 gagcttgtga cctttgtgga cgtcagggtg gtggccgcca gttgcttcat gttaattctg 660
 ctctcctatg ccaacatagt ccatgccatc ctgaagatac gcaccgctga tgggaggcgc 720
 cgggccttct ccacctgtgg ctcccaccta atcgtgggtc cagtctacta tgtccctgt 780
 attttcatct accttagggc tggtccaaa gacccctgg atggggcagc ggctgtgtt 840
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<210> 24

<211> 1060

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (17)..(892)

<400> 24

aaatgcctaa agaaga atg acc atg gaa aat tat tct atg gca gct cag ttt 52

Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe

1

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10

25/66

gtc tta gat ggt tta aca cag caa gca gag ctc cag ctg ccc ctc ttc 100

Val Leu Asp Gly Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe

15

20

25

ctc ctg ttc ctg gga atc tat gtg gtc aca gta gtg ggc aac ctg ggc 148

Leu Leu Phe Leu Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly

30

35

40

atg att ctc ctg att gca gtc agc cct cta ctt cac acc ccc atg tac 196

Met Ile Leu Leu Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr

45

50

55

60

tat ttc ctc agc agc ttg tcc ttc gtc gat ttc tgc tat tcc tct gtc 244

Tyr Phe Leu Ser Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val

65

70

75

att act ccc aaa atg ctg gtg aac ttc cta gga aag aag aat aca atc 292

Ile Thr Pro Lys Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile

80

85

90

ctt tac tct gag tgc atg gtc cag ctc ttt ttc ttt gtg gtc ttt gtg 340

Leu Tyr Ser Glu Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val

95

100

105

gtg gct gag ggt tac ctc ctg act gcc atg gca tat gat cgc tat gtt 388

Val Ala Glu Gly Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val

110	115	120	
gcc atc tgt agc cca ctg ctt tat aat gcg atc atg tcc tca tgg gtc 436			
Ala Ile Cys Ser Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val			
125	130	135	140
tgc tca ctg cta gtg ctg gct gcc ttc ttc ttg ggc ttt ctc tct gcc 484			
Cys Ser Leu Leu Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala			
	145	150	155
ttg act cat aca agt gcc atg atg aaa ctg tcc ttt tgc aaa tcc cac 532			
Leu Thr His Thr Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His			
	160	165	170
att atc aac cat tac ttc tgt gat gtt ctt ccc ctc ctc aat ctc tcc 580			
Ile Ile Asn His Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser			
175	180	185	
tgc tcc aac aca cac ctc aat gag ctt cta ctt ttt atc att gcg ggg 628			
Cys Ser Asn Thr His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly			
190	195	200	
ttt aac acc ttg gtg ccc acc cta gct gtt gct gtc tcc tat gcc ttc 676			
Phe Asn Thr Leu Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe			
205	210	215	220

27/66

atc ctc tac agc atc ctt cac atc cgc tcc tca gag ggc cgg tcc aaa 724

Ile Leu Tyr Ser Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys

225

230

235

gct ttt gga aca tgc agc tct cat ctc atg gct gtg gtg atc ttc ttt 772

Ala Phe Gly Thr Cys Ser Ser His Leu Met Ala Val Val Ile Phe Phe

240

245

250

ggg tcc att acc ttc atg tat ttc aag ccc cct tca agt aac tcc ctg 820

Gly Ser Ile Thr Phe Met Tyr Phe Lys Pro Pro Ser Ser Asn Ser Leu

255

260

265

gac cag gag aag gtg tcc tct gtg ttc tac acc acg gtg atc ccc atg 868

Asp Gln Glu Lys Val Ser Ser Val Phe Tyr Thr Thr Val Ile Pro Met

270

275

280

ctg aac cct tta ata tac agt ctg taatcacagc actttggaag gctgaggcag 922

Leu Asn Pro Leu Ile Tyr Ser Leu

285

290

ggttgcttga gtccagtttg agaccatcct ggggaacata gtgcgatctt gtttctttcc 982

actgcctaaa aacttcaatg ctcaatttta cttgcaattt cctcttcctg acatggagaa 1042

tggttgcttg gaatgttc

1060

<210> 25

<211> 1069

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (18).. (956)

<400> 25

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Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu

1 5 10

ttt att ctt gct gga tta aca gat cgt cca gag ttc tgg caa ccc ttc 98

Phe Ile Leu Ala Gly Leu Thr Asp Arg Pro Glu Phe Trp Gln Pro Phe

15 20 25

ttt ttc ctg ttc cta gtg atc tac att gtc acc atg gta ggc aac ctt 146

Phe Phe Leu Phe Leu Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu

30 35 40

ggc ttg atc act ctt ttc ggt cta aat tct cac ctc cac aca cca atg 194

Gly Leu Ile Thr Leu Phe Gly Leu Asn Ser His Leu His Thr Pro Met

45 50 55

29/66

tac tat ttc ctc ttc aat ctc tcc ttc att gat ctc tgt tac tcc tct 242

Tyr Tyr Phe Leu Phe Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser

60

65

70

75

gtt ttc act ccc aaa atg cta atg aac ttt gtg tca aaa aag aat att 290

Val Phe Thr Pro Lys Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile

80

85

90

atc tcc aat gtt ggg tgc atg act cgg ctg ttt ttc ttt ctc ttt ttc 338

Ile Ser Asn Val Gly Cys Met Thr Arg Leu Phe Phe Phe Leu Phe Phe

95

100

105

gtc atc tct gaa tgt tac atg ttg acc tca atg gca tat gat cgc tat 386

Val Ile Ser Glu Cys Tyr Met Leu Thr Ser Met Ala Tyr Asp Arg Tyr

110

115

120

gtg gcc atc tgt aat cca ttg ctg tat aag gtc acc atg tcc cat cag 434

Val Ala Ile Cys Asn Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln

125

130

135

gtc tgt tct atg ctc act ttt gct gct tac ata atg gga ttg gct gga 482

Val Cys Ser Met Leu Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly

140

145

150

155

gcc acg gcc cac acc ggg tgc atg ttt aga ctc acc ttc tgc agt gct 530

30/66

Ala Thr Ala His Thr Gly Cys Met Phe Arg Leu Thr Phe Cys Ser Ala

160

165

170

aat atc att aac cat tac ttg tgt gac ata ctc ccc ctc ctc cag ctt 578

Asn Ile Ile Asn His Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu

175

180

185

tcc tgc acc agc acc tat gtc aac gag gtg gtt gtt ctc att gtt gtg 626

Ser Cys Thr Ser Thr Tyr Val Asn Glu Val Val Val Leu Ile Val Val

190

195

200

ggt act aat atc acg gta ccc agt tgt acc atc ctc att tct tat gtt 674

Gly Thr Asn Ile Thr Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val

205

210

215

ttc att gtc act agc att ctt cat atc aaa tcc act caa gga aga tca 722

Phe Ile Val Thr Ser Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser

220

225

230

235

aaa gcc ttc agt act tgt agc tct cat gtc att gct ctg tct ctg ttt 770

Lys Ala Phe Ser Thr Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe

240

245

250

ttt ggg tca gcg gca ttc atg tat att aaa tat tct tct gga tct atg 818

Phe Gly Ser Ala Ala Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met

255

260

265

gag cag gga aaa gtt ttt tct gtt ttc tac act aat gtg gtg ccc atg 866

Glu Gln Gly Lys Val Phe Ser Val Phe Tyr Thr Asn Val Val Pro Met

270

275

280

ctc aat ccc ctc atc tac agt ttg agg aac aag gat gtc aaa gtt gca 914

Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala

285

290

295

ctg agg aaa gct ctg att aaa att cag agg aga aat ata ttc 956

Leu Arg Lys Ala Leu Ile Lys Ile Gln Arg Arg Asn Ile Phe

300

305

310

taattagaag cagtaatgat gtaaaacaat tgaaggactt caaatTTTTA ttagtgTTTT 1016

tcatgaagag atTTtgTtGt ttctacagat ggtgttatgt gtgatttaat aaa 1069

<210> 26

<211> 1069

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (18).. (956)

<400> 26

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Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu

1

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ttt att ctt gct gga tta aca gat cgt cca gag ttc cgg caa ccc ctc 98

Phe Ile Leu Ala Gly Leu Thr Asp Arg Pro Glu Phe Arg Gln Pro Leu

15

20

25

ttt ttc ctg ttt cta gtg atc tac att gtc acc atg gta ggc aac ctt 146

Phe Phe Leu Phe Leu Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu

30

35

40

ggc ttg atc att ctt ttc ggt cta aat tct cac ctc cac aca cca atg 194

Gly Leu Ile Ile Leu Phe Gly Leu Asn Ser His Leu His Thr Pro Met

45

50

55

tac tat ttc ctc ttc aat ctc tcc ttc att gat ctc tgt tac tcc tct 242

Tyr Tyr Phe Leu Phe Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser

60

65

70

75

gtt ttc act ccc aaa atg cta atg aac ttt gta tca aaa aag aat att 290

Val Phe Thr Pro Lys Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile

80

85

90

atc tcc tat gtt ggg tgc atg act cag ctg ttt ttc ttt ctc ttt ttt 338

Ile Ser Tyr Val Gly Cys Met Thr Gln Leu Phe Phe Phe Leu Phe Phe

95

100

105

gtc atc tct gaa tgc tac ata ttg acc tca atg gca tat gat cgc tat 386

Val Ile Ser Glu Cys Tyr Ile Leu Thr Ser Met Ala Tyr Asp Arg Tyr

110

115

120

gtg gcc atc tgt aat cca ttg ctg tat aag gtc acc atg tcc cat cag 434

Val Ala Ile Cys Asn Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln

125

130

135

gtc tgt tct atg ctc act ttt gct gct tac ata atg gga ttg gct gga 482

Val Cys Ser Met Leu Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly

140

145

150

155

gcc acg gcc cac acc ggg tgc atg ctt aga ctc acc ttc tgc agt gct 530

Ala Thr Ala His Thr Gly Cys Met Leu Arg Leu Thr Phe Cys Ser Ala

160

165

170

aat atc atc aac cat tac ttg tgt gac ata ctc ccc ctc ctc cag ctt 578

Asn Ile Ile Asn His Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu

175

180

185

tcc tgc acc agc acc tat gtc aac gag gtg gtt gtt ctc att gtt gtg 626

Ser Cys Thr Ser Thr Tyr Val Asn Glu Val Val Val Leu Ile Val Val

190	195	200	
ggt att aat atc atg gta ccc agt tgt acc atc ctc att tct tat gtt 674			
Gly Ile Asn Ile Met Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val			
205	210	215	
ttc att gtc act agc att ctt cat atc aaa tcc act caa gga aga tca 722			
Phe Ile Val Thr Ser Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser			
220	225	230	235
aaa gcc ttc agt act tgt agc tct cat gtc att gct ctg tct ctg ttt 770			
Lys Ala Phe Ser Thr Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe			
240	245	250	
ttt ggg tca gcg gca ttc atg tat att aaa tat tct tct gga tct atg 818			
Phe Gly Ser Ala Ala Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met			
255	260	265	
gag cag gga aaa gtt tct tct gtt ttc tac act aat gtg gtg ccc atg 866			
Glu Gln Gly Lys Val Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met			
270	275	280	
ctc aat cct ctc atc tac agt ttg agg aac aag gat gtc aaa gtt gca 914			
Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala			
285	290	295	

ctg agg aaa gct ctg att aaa att cag aga aga aat ata ttc 956

Leu Arg Lys Ala Leu Ile Lys Ile Gln Arg Arg Asn Ile Phe

300

305

310

taattagaag cagtaataat gtaaaacgat tgaagaactt taaattttta ttagtgtgtt 1016

ccatgaagag attttggtgt ttctacagat ggtggtatgt gtgatttaaat aaa 1069

<210> 27

<211> 976

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19).. (945)

<400> 27

acagctcgcc aagagaga atg act ctg aga aac agc tcc tca gtg act gag 51

Met Thr Leu Arg Asn Ser Ser Ser Val Thr Glu

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10

ttt atc ctt gtg gga tta tca gaa cag cca gag ctc cag ctc cct ctt 99

Phe Ile Leu Val Gly Leu Ser Glu Gln Pro Glu Leu Gln Leu Pro Leu

15

20

25

ttc ctt cta ttc tta ggg atc tat gtg ttc act gtg gtg ggc aac ttg 147

Phe Leu Leu Phe Leu Gly Ile Tyr Val Phe Thr Val Val Gly Asn Leu

30

35

40

ggc ttg atc acc tta att ggg ata aat cct agc ctt cac acc ccc atg 195

Gly Leu Ile Thr Leu Ile Gly Ile Asn Pro Ser Leu His Thr Pro Met

45

50

55

tac ttt ttc ctc ttc aac ttg tcc ttt ata gat ctc tgt tat tcc tgt 243

Tyr Phe Phe Leu Phe Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Cys

60

65

70

75

gtg ttt acc ccc aaa atg ctg aat gac ttt gtt tca gaa agt atc atc 291

Val Phe Thr Pro Lys Met Leu Asn Asp Phe Val Ser Glu Ser Ile Ile

80

85

90

tct tat gtg gga tgt atg act cag cta ttt ttc ttc tgt ttc ttt gtc 339

Ser Tyr Val Gly Cys Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val

95

100

105

aat tct gag tgc tat gtg ttg gta tca atg gcc tat gat cgc tat gtg 387

Asn Ser Glu Cys Tyr Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val

110

115

120

gcc atc tgc aac ccc ctg ctc tac atg gtc acc atg tcc cca agg gtc 435

Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Arg Val

125

130

135

tgc ttt ctg ctg atg ttt ggt tcc tat gtg gta ggg ttt gct ggg gcc 483

Cys Phe Leu Leu Met Phe Gly Ser Tyr Val Val Gly Phe Ala Gly Ala

140

145

150

155

atg gcc cac act gga agc atg ctg cga ctg acc ttc tgt gat tcc aac 531

Met Ala His Thr Gly Ser Met Leu Arg Leu Thr Phe Cys Asp Ser Asn

160

165

170

gtc att gac cat tat ctg tgt gac gtt ctc ccc ctc ttg cag ctc tcc 579

Val Ile Asp His Tyr Leu Cys Asp Val Leu Pro Leu Leu Gln Leu Ser

175

180

185

tgc acc agc acc cat gtc agt gag ctg gta ttt ttc att gtt gtt gga 627

Cys Thr Ser Thr His Val Ser Glu Leu Val Phe Phe Ile Val Val Gly

190

195

200

gta atc acc atg cta tcc agc ata agc atc gtc atc tct tac gct ttg 675

Val Ile Thr Met Leu Ser Ser Ile Ser Ile Val Ile Ser Tyr Ala Leu

205

210

215

ata ctc tcc aac atc ctc tgt att cct tct gca gag ggc aga tcc aaa 723

Ile Leu Ser Asn Ile Leu Cys Ile Pro Ser Ala Glu Gly Arg Ser Lys

220

225

230

235

gcc ttt agc aca tgg ggc tcc cac ata att gct gtt gct ctg ttt ttt 771

Ala Phe Ser Thr Trp Gly Ser His Ile Ile Ala Val Ala Leu Phe Phe

240

245

250

ggg tca ggg aca ttc acc tac tta aca aca tct ttt cct ggc tct atg 819

Gly Ser Gly Thr Phe Thr Tyr Leu Thr Thr Ser Phe Pro Gly Ser Met

255

260

265

aac cat ggc aga ttt gcc tca gtc ttt tac acc aat gtg gtt ccc atg 867

Asn His Gly Arg Phe Ala Ser Val Phe Tyr Thr Asn Val Val Pro Met

270

275

280

ctt aac cct tcg atc tac agt ttg agg aat aag gat gat aaa ctt gcc 915

Leu Asn Pro Ser Ile Tyr Ser Leu Arg Asn Lys Asp Asp Lys Leu Ala

285

290

295

ctg ggc aaa acc ctg aag aga gtg ctc ttc taatgggtct cttcatatca 965

Leu Gly Lys Thr Leu Lys Arg Val Leu Phe

300

305

ctggcaaccg a

976

<210> 28

<211> 292

<212> PRT

<213> Homo sapiens

<400> 28

Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe Val Leu Asp Gly

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15

Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu

20

25

30

Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly Met Ile Leu Leu

35

40

45

Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser

50

55

60

Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys

65

70

75

80

Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile Leu Tyr Ser Glu

85

90

95

Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val Val Ala Glu Gly

100

105

110

Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser

115

120

125

Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val Cys Ser Leu Leu

130

135

140

Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala Leu Thr His Thr

145

150

155

160

Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His

165

170

175

Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr

180

185

190

His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu

195

200

205

Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser

210

215

220

Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr

225

230

235

240

Cys Ser Ser His Leu Met Ala Val Val Ile Phe Phe Gly Ser Ile Thr

245

250

255

Phe Met Tyr Phe Lys Pro Pro Ser Ser Asn Ser Leu Asp Gln Glu Lys

260

265

270

Val Ser Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu

275

280

285

Ile Tyr Ser Leu

290

<210> 29

<211> 313

<212> PRT

<213> Homo sapiens

<400> 29

Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu Phe Ile Leu Ala Gly

1

5

10

15

Leu Thr Asp Arg Pro Glu Phe Trp Gln Pro Phe Phe Phe Leu Phe Leu

20

25

30

Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu Gly Leu Ile Thr Leu

35

40

45

Phe Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Phe

50 55 60

Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys

65 70 75 80

Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile Ile Ser Asn Val Gly

 85 90 95

Cys Met Thr Arg Leu Phe Phe Phe Leu Phe Phe Val Ile Ser Glu Cys

 100 105 110

Tyr Met Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn

 115 120 125

Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln Val Cys Ser Met Leu

 130 135 140

Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly Ala Thr Ala His Thr

145 150 155 160

Gly Cys Met Phe Arg Leu Thr Phe Cys Ser Ala Asn Ile Ile Asn His

 165 170 175

Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr

 180 185 190

Tyr Val Asn Glu Val Val Val Leu Ile Val Val Gly Thr Asn Ile Thr

195

200

205

Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser

210

215

220

Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr

225

230

235

240

Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala

245

250

255

Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val

260

265

270

Phe Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile

275

280

285

Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Lys Ala Leu

290

295

300

Ile Lys Ile Gln Arg Arg Asn Ile Phe

305

310

<211> 313

<212> PRT

<213> Homo sapiens

<400> 30

Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu Phe Ile Leu Ala Gly

1 5 10 15

Leu Thr Asp Arg Pro Glu Phe Arg Gln Pro Leu Phe Phe Leu Phe Leu

20 25 30

Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu Gly Leu Ile Ile Leu

35 40 45

Phe Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Phe

50 55 60

Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys

65 70 75 80

Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile Ile Ser Tyr Val Gly

85 90 95

Cys Met Thr Gln Leu Phe Phe Phe Leu Phe Phe Val Ile Ser Glu Cys

100 105 110

Tyr Ile Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn

115

120

125

Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln Val Cys Ser Met Leu

130

135

140

Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly Ala Thr Ala His Thr

145

150

155

160

Gly Cys Met Leu Arg Leu Thr Phe Cys Ser Ala Asn Ile Ile Asn His

165

170

175

Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr

180

185

190

Tyr Val Asn Glu Val Val Val Leu Ile Val Val Gly Ile Asn Ile Met

195

200

205

Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser

210

215

220

Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr

225

230

235

240

Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala

245

250

255

Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val

260

265

270

Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile

275

280

285

Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Lys Ala Leu

290

295

300

Ile Lys Ile Gln Arg Arg Asn Ile Phe

305

310

<210> 31

<211> 309

<212> PRT

<213> Homo sapiens

<400> 31

Met Thr Leu Arg Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Val Gly

1

5

10

15

Leu Ser Glu Gln Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu

20

25

30

Gly Ile Tyr Val Phe Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu

35

40

45

Ile Gly Ile Asn Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Phe

50

55

60

Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Cys Val Phe Thr Pro Lys

65

70

75

80

Met Leu Asn Asp Phe Val Ser Glu Ser Ile Ile Ser Tyr Val Gly Cys

85

90

95

Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu Cys Tyr

100

105

110

Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro

115

120

125

Leu Leu Tyr Met Val Thr Met Ser Pro Arg Val Cys Phe Leu Leu Met

130

135

140

Phe Gly Ser Tyr Val Val Gly Phe Ala Gly Ala Met Ala His Thr Gly

145

150

155

160

Ser Met Leu Arg Leu Thr Phe Cys Asp Ser Asn Val Ile Asp His Tyr

165

170

175

Leu Cys Asp Val Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr His

180

185

190

Val Ser Glu Leu Val Phe Phe Ile Val Val Gly Val Ile Thr Met Leu

195

200

205

Ser Ser Ile Ser Ile Val Ile Ser Tyr Ala Leu Ile Leu Ser Asn Ile

210

215

220

Leu Cys Ile Pro Ser Ala Glu Gly Arg Ser Lys Ala Phe Ser Thr Trp

225

230

235

240

Gly Ser His Ile Ile Ala Val Ala Leu Phe Phe Gly Ser Gly Thr Phe

245

250

255

Thr Tyr Leu Thr Thr Ser Phe Pro Gly Ser Met Asn His Gly Arg Phe

260

265

270

Ala Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Ser Ile

275

280

285

Tyr Ser Leu Arg Asn Lys Asp Asp Lys Leu Ala Leu Gly Lys Thr Leu

290

295

300

Lys Arg Val Leu Phe

305

<210> 32

<211> 762

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (17)..(760)

<400> 32

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Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe

1

5

10

gtc tta gat ggt tta aca cag caa gca gag ctc cag ctg ccc ctc ttc 100

Val Leu Asp Gly Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe

15

20

25

ctc ctg ttc ctg gga atc tat gtg gtc aca gta gtg ggc aac ctg ggc 148

Leu Leu Phe Leu Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly

30

35

40

atg att ctc ctg att gca gtc agc cct cta ctt cac acc ccc atg tac 196

Met Ile Leu Leu Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr

45 50 55 60

tat ttc ctc agc agc ttg tcc ttc gtc gat ttc tgc tat tcc tct gtc 244

Tyr Phe Leu Ser Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val

65 70 75

att act ccc aaa atg ctg gtg aac ttc cta gga aag aag aat aca atc 292

Ile Thr Pro Lys Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile

80 85 90

ctt tac tct gag tgc atg gtc cag ctc ttt ttc ttt gtg gtc ttt gtg 340

Leu Tyr Ser Glu Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val

95 100 105

gtg gct gag ggt tac ctc ctg act gcc atg gca tat gat cgc tat gtt 388

Val Ala Glu Gly Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val

110 115 120

gcc atc tgt agc cca ctg ctt tat aat gcg atc atg tcc tca tgg gtc 436

Ala Ile Cys Ser Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val

125 130 135 140

tgc tca ctg cta gtg ctg gct gcc ttc ttc ttg ggc ttt ctc tct gcc 484

Cys Ser Leu Leu Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala

145 150 155

ttg act cat aca agt gcc atg atg aaa ctg tcc ttt tgc aaa tcc cac 532

Leu Thr His Thr Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His

160

165

170

att atc aac cat tac ttc tgt gat gtt ctt ccc ctc ctc aat ctc tcc 580

Ile Ile Asn His Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser

175

180

185

tgc tcc aac aca cac ctc aat gag ctt cta ctt ttt atc att gcg ggg 628

Cys Ser Asn Thr His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly

190

195

200

ttt aac acc ttg gtg ccc acc cta gct gtt gct gtc tcc tat gcc ttc 676

Phe Asn Thr Leu Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe

205

210

215

220

atc ctc tac agc atc ctt cac atc cgc tcc tca gag ggc cgg tcc aaa 724

Ile Leu Tyr Ser Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys

225

230

235

gct ttt gga aca tgc agc tct cat ctc atg gct gtg gt 762

Ala Phe Gly Thr Cys Ser Ser His Leu Met Ala Val

240

245

<210> 33

<211> 248

<212> PRT

<213> Homo sapiens

<400> 33

Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe Val Leu Asp Gly

1 5 10 15

Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu

20 25 30

Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly Met Ile Leu Leu

35 40 45

Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser

50 55 60

Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys

65 70 75 80

Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile Leu Tyr Ser Glu

85 90 95

Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val Val Ala Glu Gly

100 105 110

Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser

115

120

125

Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val Cys Ser Leu Leu

130

135

140

Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala Leu Thr His Thr

145

150

155

160

Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His

165

170

175

Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr

180

185

190

His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu

195

200

205

Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser

210

215

220

Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr

225

230

235

240

Cys Ser Ser His Leu Met Ala Val

245

<210> 34

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 34

gaagagcagt gaggtccat gttaagg

27

<210> 35

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 35

cagcagcttg tccttcgtcg atttctgc

28

<210> 36

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 36

gctagggtgg gcaccaaggt gttaaacc

29

<210> 37

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 37

tgcaaaagga cagtttcac atggcac

27

<210> 38

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 38

caaagaactc acccaaattc ctacagct

28

<210> 39

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 39

catggtaggc aaccttggct tgatcac

27

<210> 40

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 40

gtttattaaa tcacacataa caccatctg

29

<210> 41

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 41

cagagacaga gcaatgacat gagagctac

29

<210> 42

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 42

caaagaactc acccaaattc ctacagcc

28

<210> 43

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 43

catggtaggc aaccttggct tgatcat

27

<210> 44

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 44

gtttattaaa tcacacataa caccatctg

29

<210> 45

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 45

cagagacaga gcaatgacat gagagctac

29

<210> 46

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 46

ccagacagct cgccaagaga gaatgac

27

<210> 47

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 47

cctttataga tctctgttat tcctgtgtg

29

<210> 48

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 48

tcggttgcca gtgatatgaa gagaccc

27

<210> 49

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 49

ggctttggat ctgccctctg cagaagg

27

<210> 50

<211> 450

<212> DNA

<213> Homo sapiens

<400> 50

cagcagcttg tccttcgtcg atttctgcta ttctctgtc attactccca aaatgctggt 60

gaacttccta ggaaagaaga atacaatcct ttactctgag tgcattgtcc agctcttttt 120

ctttgtggtc tttgtggtgg ctgagggtta cctcctgact gccatggcat atgattgcta 180

tggtgccatc tgtagccac tgctttataa tgcatcatg tcctcatggg tctgtcact 240

gctagtgtg gctgccttct tcttgggctt tctctctgcc ttgactcata caagtccat 300

gatgaaactg tccttttgca aatccacat tatcaacct tacttctgtg atgttcttcc 360

cctcctcaat ctctcctgct ccaacacaca cctcaatgag cttctacttt ttatcattgc 420

ggggtttaac accttggtgc ccaccctagc

450

<210> 51

<211> 637

<212> DNA

<213> Homo sapiens

<400> 51

catggtaggc aaccttggct tgatcactct tttegggtcta aattctcacc tccacacacc 60

aatgtactat ttctctttca atctctcctt cattgatctc tgttactcct ctgtttttcac 120

tcccaaaatg ctaatgaact ttgtgtcaaa aaagaatatt atctccaatg ttgggtgcat 180

gactcggctg tttttctttc tctttttcgt catctctgaa tgttacatgt tgacctcaat 240

ggcatatgat cgctatgtgg ccatctgtaa tccattgctg tataaggcca ccatgtccca 300

tcaggctctgt tctatgctca cttttgctgc ttacataatg ggattggctg gagccacggc 360

ccacacggg tgcatgttta gactcacctt ctgcagtgt aatatcatta accattactt 420

gtgtgacata ctccccctcc tccagctttc ctgcaccagc acctatgtca acgaggtggg 480

tgttctcatt gttgtgggta ctaatatcac ggtaccagc tgtaccatcc tcatttttta 540

tgttttcatt gtcactagca ttcttcatat caaatccact caaggaagat caaaagcctt 600

cagtacttgt agctctcatg tcattgctct gtctctg

637

<210> 52

<211> 637

<212> DNA

<213> Homo sapiens

<400> 52

catggtaggc aaccttggct tgatcattct tttcggctca aattctcacc tccacacacc 60

aatgtactat ttctcttcca atctctcctt cattgatctc tgttactcct ctgttttcac 120

tcccaaaatg ctaatgaact ttgtatcaaa aaagaatatt atctcctatg ttgggtgcat 180

gactcagctg tttttctttc tcttttttgt catctctgaa tgctacatat tgacctcaat 240

ggcatatgat cgctatgtgg ccatctgtaa tccattgctg tataaggcca ccatgtccca 300

tcaggctctgt tctatgctca cttttgctgc ttacataatg ggattggctg gagccacggc 360

ccacaccggg tgcatgctta gactcacctt ctgcagtgt aatatcatca accattactt 420

gtgtgacata ctccccctcc tccagctttc ctgcaccagc acctatgtca acgaggtggt 480

tgtttctcatt gttgtgggta ttaatatcat ggtaccagc tgtaccatcc tcattttcta 540

tgttttcatt gtcactagca ttcttcatat caaatccact caaggaagat caaaagcctt 600

cagtacttgt agctctcatg tcattgctct gtctctg 637

<210> 53

<211> 509

<212> DNA

<213> Homo sapiens

<400> 53

cctttataga tctctgttat tcctgtgtgt ttacccccaa aatgctgaat gactttgttt 60

cagaaagtat catctcttat gtgggatgta tgactcagct atttttcttc tgtttctttg 120

tcaattctga gtgctatgtg ttggtatcaa tggcctatga togctatgtg gccatctgca 180

acccctgct ctacatgggc accatgtccc caagggtctg cttctgctg atgtttggtt 240

cctatgtggt agggtttgct ggggccatgg cccacactgg aagcatgctg cgactgacct 300

tctgtgattc caacgtcatt gaccattatc tgtgtgacgt tctccccctc ttgcagctct 360

cctgcaccag caccatgtc agtgagctgg tatttttcat tgttgttgga gtaatcacca 420

tgctatccag cataagcatc gtcattcttt acgctttgat actctccaac atcctctgta 480

ttccttctgc agagggcaga tccaaagcc

509